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SEQUENCE LISTING

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<120> RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

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<141> 2001-05-24

<150> US 09/580,515
<151> 2000-05-25

<150> US 09/318,528
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<150> US 09/291,931
<151> 1999-04-13

<150> US 09/259,214
<151> 1999-03-01

<150> US 08/910,798
<151> 1997-08-13

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<170> PatentIn version 3.1

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ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt 96
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
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gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg 144
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr

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aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp 100 105 110			336
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agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg agc gcc Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala 210 215 220			672
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gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His 260 265 270			816
aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser 275 280 285			864

cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat 912
 Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His
 290 295 300

cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg 960
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
 305 310 315 320

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 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
 325 330 335

gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt 1056
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
 340 345 350

ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag 1104
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
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tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat 1152
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
 370 375 380

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 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
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ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca 1248
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Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
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Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
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Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
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Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
 85 90 95

Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
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Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
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Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
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Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
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 195 200 205

Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
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Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
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Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
 245 250 255

Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
 260 265 270

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Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His

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Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
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Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
 325 330 335

Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
 340 345 350

Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
 355 360 365

Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
 370 375 380

Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
 385 390 395 400

Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
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Arg Ser His His His His His His
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<220>
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20           25           30

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50 55 60

Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
65 70 75 80

Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
85 90 95

Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
100 105 110

Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
115 120 125

Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
130 135 140

Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
145 150 155 160

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165 170 175

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180 185 190

Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
195 200 205

Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
210 215 220

Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
225 230 235 240

Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
245 250 255

Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
260 265 270

Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
 275 280 285

Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His
 290 295 300

Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
 305 310 315 320

Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
 325 330 335

Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
 340 345 350

Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
 355 360 365

Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
 370 375 380

Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
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<212> PRT

<213> Artificial Sequence

<220>

<223> Modified phytase

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Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
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Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
35 40 45

Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
50 55 60

Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
65 70 75 80

Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys
85 90 95

Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
100 105 110

Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
115 120 125

Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
130 135 140

Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
145 150 155 160

Asn Val Thr Asp Ala Ile Leu Glu Ala Gly Gly Ser Ile Ala Asp Phe
165 170 175

Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
180 185 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
195 200 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
210 215 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu

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Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn						
		260		265		270
Ala Gln Phe Asp Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg Ala						
		275		280		285
Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro Pro						
		290		295		300
Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe Ile						
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Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu Leu						
		325		330		335
Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly Glu						
		340		345		350
Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp Ile						
		355		360		365
Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys Thr						
		370		375		380
Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu Ala						
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Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly Phe						
		405		410		415
Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu						
		420		425		430